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LOCUS AX140883

DEFINITION Sequence 373 from Patent WO0134802.

ACCESSION AX140883

VERSION AX140883.1 GI:14280986

KEYWORDS

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PAT 31-MAY-2001

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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1155)
AUTHORS
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelly,X.A. and Wang,A.
TITLE
Compositions and methods for the therapy and diagnosis of prostate
cancer
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Patent: WO 0134802-A 373 17-MAY-2001;
CORIXA CORPORATION (US)
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LOCUS AX200743

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ACCESSION AX200743

VERSION AX200743.1 GI:15390636

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1155)

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Rether,M.W., Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: WO 0151633-A 373 19-JUL-2001; CORIXA CORPORATION (US)

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 REFERENCE  
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 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,X.,  
 Kalos,M.D., Fanger,G.R., Rether,M.W., Stolk,J.A., Day,C.H.,  
 Vedyick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.T.  
 and Henderson,R.A.  
 TITLE Compositions and methods for the therapy and diagnosis of prostate  
 cancer  
 JOURNAL Patent: WO 0173032-A 373 04-OCT-2001;  
 CORIXA CORPORATION (US)  
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ACCESSION AX282956
VERSION AX282956.1 GI:16609896
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REFERENCE
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AUTHORS Houghton, R.L., Dillon, D.C., Molesh, D.A., Xu, J., Zehentner, B. and
Pearling, D.H.
TITLE Methods, compositions and kits for the detection and monitoring of
breast cancer
JOURNAL Patent: WO 0175171-A 5 11-OCT-2001;
CORIXA CORPORATION (US)
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LOCUS AX316964
DEFINITION Sequence 301 from Patent WO0190152.
ACCESSION AX316964
VERSION AX316964.1 GI:17900043
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (sites)
Fudakis, J.N., Reed, S.G., Smith, J.M., Misher, L.E., Dillon, D.C.,
Retter, M.W., Wang, A., Skelley, J.A., Haddock, S.L. and Day, C.H.,
Compositions and methods for the therapy and diagnosis of breast
cancer
Patent: WO 0190152-A 301 29-NOV-2001;
JOURNAL CORIXA CORPORATION (US)
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LOCUS AX316986 1590 bp DNA linear PAT 14-DEC-2001

DEFINITION Sequence 323 from Patent WO0190152.

ACCESSION AX316986

VERSION AX316986.1 GI:17900055

KEYWORDS

SOURCE

ORGANISM

human.  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

Patent: WO 0190152-A 323 29-NOV-2001;

CORIXA CORPORATION (US)

FEATURES

Location/Qualifiers

Source

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LOCUS AX316991 1155 bp DNA linear PAT 14-DEC-2001

DEFINITION Sequence 328 from Patent WO0190152.

ACCESSION AX316991

VERSION AX316991.1 GI:17900058

KEYWORDS

SOURCE human.

## ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (sites)  
Frudakis, T.N., Reed, S.G., Smith, J.M., Misher, L.E., Dillon, D.C.,  
Reiter, M.W., Wang, Y.A., Harlocker, S.L., and Day, C.H.  
Compositions and methods for the therapy and diagnosis of breast  
cancer  
Patent: WO 0190152-A 328 29-NOV-2001;

## JOURNAL

CORIXA CORPORATION (US)

## FEATURES

Location/Qualifiers

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DEFINITION Sequence 374 from Patent WO0125272.
ACCESSION AX106593
VERSION AX106593.1 GI:13922264
KEYWORDS
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ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu, Y., Skelky, Y.A., Reed, S.G. and Cheever, M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0125272-A 374 12-APR-2001;
CORIXA CORPORATION (US)
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LOCUS AX140884 2000 bp DNA linear PAT 31-MAY-2001

DEFINITION Sequence 374 from Patent WO0134802.

ACCESSION AX140884

VERSION AX140884.1 GI:14280987

KEYWORDS

SOURCE

ORGANISM

human.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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ORIGIN

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Ratio: 5.383 Gaps: 0

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REFERENCE
1 (bases 1 to 2000)
XU,J., DILLON,D.C., MITCHAM,J.L., HARLOCKER,S.L., JIANG,Y.,
REED,S.G., KALOS,M.D., FANGER,G.R., DAY,C.H., RETTER,M.W.,
STOLK,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
cancer. WO 0151633-A 374 19-JUL-2001;
JOURNAL CORIXA CORPORATION (US)
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ACCESSION AX267400
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REFERENCE
1 (sites)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Reiter,M.W., Stolk,V.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.T.
and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer.
Patent: WO 0173032-A 374 04-OCT-2001;
CORIXA CORPORATION (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (sites)
AUTHORS Houghton,R.L., Dillon,D.C., Molesh,D.A., Xu,J., Zehentner,B. and
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Persing,D.H.
Methods, compositions and kits for the detection and monitoring of
Breast cancer
Patent: WO 0175171-A 6 11-OCT-2001;
JOURNAL CORIXA CORPORATION (US)
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REFERENCE
AUTHORS Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate
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JOURNAL Patent: WO 0125272-A 375 12-Apr-2001;
CORIXA CORPORATION (US)
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51 ATTGGTCTCAGAGCAAGATGGCAAGTGTCTGCTGCTGCTCCCT 100
34 yscysargglyserglysserasnvalglythrserylasp 50
101 gctgcagagagacgcacagacacgcttcttgagacacacgac 150
51 Aspseralmetlysthrleuargserlysmetglystpcysarghi 67
151 GACTCTGCTATGAAGACACTCAGAGCAAGATGGCAAGTGGCCGCA 200
67 scyspheprocyscysargglyserglysserasnvalglyalsarg 84
201 CTGCTTCCCTGCTGCAGGGGAGTGGCAAGACACGTGGCGCTTCTG 250
84 lypshisaspaspseralmetlysthrleuargasnlysmetglylys 100
251 GAGACACGACGACTCTGCTATGAAGACACTCAGAAACAAGATGGCAAG 300
101 Trpcyscyshtscyspheprocyscysargglyserglysserlyst 117
301 TGGTGTGCTGCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGNCAAGT 350
117 lglyalatrpglyaspptyraspaspseralaphemetgluproargtyr 134
351 GGGCGCTTGGGGAGACTACGATCAGAGTGCCTTCATGAGCCAGGTACC 400
134 lsvlaargglygluasplleuaspllystleuhtsargalatrptpgly 150
401 ACGTCCGTGGAAGAATCTGCAACAAGCTCCACAGAGCTGCTGCTGGGT 450
151 lysvalproarglyaspplleuilevalmetleuargspthraspylas 167
451 AAAGTCCCGAAGAAAGGATCTCATGCTCAGGACACTGACCTGAA 500
167 nllyslaspllysglnlystgthrleuhtsleuallaseralasp 184
501 CAAGAAGACAGCAAAAGAGAGCTGCTACACTGCGCTCGCCCAATG 550
184 lypasnergluvallyslleuleuleuaspargargcysglnleuasn 200
551 GGAATTCAGAAAGTAGTAAACTCCTGCTGCAAGACAGATGTCAACTAAT 600
201 Valleuaspanlystysargthrleuilelysalavalglnycsgl 217
601 GTCTTGACAAACAAGAGAGAGCTGTGATTAAGCCGTACAAATGCCA 650
217 ngluasplucysalaleuhtleuleuenglhtsglythraspproasn 234
651 GGAAGATGAATGTGCTTAATGTTGCGAACAATGGCACATGCCAAATA 700
234 leproaspglutyrglyasnthrthrlleuhtstyrallatieryrasn 250
701 TTCACAGATGAGTATGAATAATCACACTGCTGCAACCGCTATCTATGA 750
251 Asplysleumetalysalaleuleuleuhtyrglyalaspillegluse 267
751 GATAAATTAATGCGCAAGCACTGCTCTTATATGCTGATATCGAATC 800
267 rlyasasnlyshisglyleuthrproleuleuleuagllyvalhisgln 284
801 AAAAAACACAGATGGCTCTCACACACACTGTTGCTGCTACATGACACAA 850
284 ysglnglnvallyslpheleuilelystlysalasnleuasnal 300
851 AACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAATATGCA 900
301 leuasprargtyrglyargthrleuileleuallvalcysgysglyse 317
|||||

```

```

901 CTGATACATATGCAAGACACTGCTCTCACTTGTCTGTATGTTGATC 950
317 rAlaserllevalserleuleuleuenglhtasnllaspvalserberg 334
951 AGCAATATATAGTCAGCGCTTCTACTGAGCAAAATATATGATATCTTCTC 1000
334 lnaspleuserglylnthrleuarglutyralavalserberhis 350
1001 AAGATCTATCTGACAGACGCGCAGAGATATGCTGTTCTATGATCATAT 1050
351 Hisvalillecysglnleuleuseraptyrlysglnlysglnmetleu 367
1051 CATGCTATTGCGCAGTTACTTCTGACTACAAAGAAAAACAAGATGCTAAA 1100
367 slieserergluasnserasnprogluasnvalserargthrasn 384
1101 AATCTCTTCGAAACAGCAATCCAGAAATGTCTCAGAACCAAGATTA 1150
384 ys 384
1151 AA 1152

seq_name: /SIDS1/gcdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA06598
seq_documentation_block:
ID AAA06598 standard; cDNA; 1155 BP.
XX
AC AAA06598;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:373.
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PE 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
DR WPI: 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein -
XX
PS Claim 50; Page 222; 263pp; English.
XX

The present invention describes isolated polypeptides, comprising an
immunogenic portion of a prostate tumour protein (pnp). The polypeptides
and polynucleotides encoding them have cytostatic activity and can be
used in vaccines and in gene therapy. The polypeptides and
polynucleotides encoding them, antigen presenting cells which express
the polypeptides, antibodies against the polypeptides and vaccines
comprising them can be used for inhibiting the development of prostate
cancer in a patient. The polypeptides can be used to generate antibodies
or anti-idiotypic antibodies for passive immuno therapy. A portion of
the polynucleotides encoding the polypeptides can be used as a probe or

```

CC to modulate the expression of the polypeptides. AA06241 to AA06691 and  
CC AA082000 to AA082020 represent sequences used in the exemplification of  
the present invention.

XX Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

# alignment\_scores:

Quality: 2064.00 Length: 384  
Ratio: 5.375 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-810-936-304 x AA06598 ..

Align seg 1/1 to: AA06598 from: 1 to: 1155

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1 MetValValGluValAspSerMetProAlaIaIaSerSerValLysLysPR 17
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1 ATGGTGGTGAAGGTATATTCATGCGGCTCTCTCTGTAAGAAAGCC 50
17 opheGlyLeuArgSerLysMetGlyLysTrpCysArgCysPheProC 34
|||||
51 ATTGGTCTCAGGAGCAAGATGGGCAAGTGGTGGCTGGCTGCCCT 100
34 yscysArgGlySerGlyLysSerAsnValGlyThrSerGlyAspHisasp 50
|||||
101 GCTGCAAGGAGAGGCGCAAGACAGACGTCGTCGAGACACACAC 150
51 AspSerAlaMetLysThrLeuArgSerLysMetGlyLysTrpCysArgH 67
|||||
151 GACTCTCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCCA 200
67 scysPheProCysArgLysGlySerGlyLysSerAsnValGlyAlaSerG 84
|||||
201 CTGCTTCCTGCTGCGAGGGAGTGGCAAGCAACGTGGGCGCTTCTG 250
84 LysAspHisAspSerAlaMetLysThrLeuArgAsnLysMetLysLys 100
|||||
251 GAGACCCAGACGACTGCTATGACAGACACTCAGAGCAAGATGGGCAAG 300
101 TrpCysCysHisCysPheProCysCysArgGlySerGlyLysSerLysVal 117
|||||
301 TGGTGGTGGCAGCTGCTCCCTGCTGCAAGGGAGGGGCAAGACAGCAAGT 350
117 IGlyAlaIaIaTrpGlyAspTrpLysAspSerAlaPheMetGluProArgLys 134
|||||
351 GGGGCGCTGGGAGACTACGATGACAGTGTCTTCATGGAGCCAGGTGCC 400
134 IsValArgGlyGluAspLeuAspLysLeuHisArgAlaIaIaIaTrpGly 150
|||||
401 ACGTCCGCGGAGAAAGATCTGGACAGCTCCACAGAGCTCCGCGGGGT 450
151 LysValIaIaProArgLysAspLeuIleValMetLeuArgAspThrAspValAs 167
|||||
451 AAAGTCCCGCAAGAAAGATCTCATGTCATGCTCAGGAGACATGAGCTGAA 500
167 nLysLysAspLysGlnLysArgThrAlaLeuHisLysLeuAlaSerAlaAsnG 184
|||||
501 CAAGAGAGACAAAGCAAGAGAGACTGCTACATCTGGGCTGGCCAAATG 550
184 LysAsnSerGluValValLysLeuLeuLeuAspArgArgGlySerGlnLeuAsn 200
|||||
551 GGAATTCAGAGTAGTAAACTCCTGCTGGACAGAGAGTGTCAACTTATAT 600
201 ValLeuAspAsnLysLysArgThrAlaLeuIleLysAlaValaGlnCysG 217
|||||
601 GTCTCTGCAACAACAAAGAGAGACAGCTGTGATAAAGGCCGTACATGCA 650
217 nGluAspGlyCysAlaLeuMetLeuGlnHisGlyLysTrpAspProAsn 234
|||||
651 GGAAGATGAATGTGCTTAATGTGCTGGACAGTGGCACTGATCAAAATA 700

```

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234 leProAspGluTrpGlyAsnThrThrLeuHisTyrAlaIleTyrAsnGlu 250
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701 TTCAGATGAGTAGTAAAGAAATACACACTGCACTACGCTATCTATTAAGAA 750
251 AspLysLeuMetAlaLysAlaLeuLeuLeuTyrGlyAlaAspIleGluSe 267
|||||
751 GATAAATTTAATGGCCAAAGCAGCTGCTTATATGTGTGCTGATATCGAATC 800
267 rLysAsnLysHisGlyLeuThrProLeuLeuLeuGlyValHisGlnL 284
|||||
801 AAAAACAAGCATGGCTTCACACACTGTTACTTGTTACTTGTTACTGATGAC 850
284 yscGlnGlnValLysPheLeuIleLysLysAlaLeuAsnLysAla 300
|||||
851 AACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCAATTTAATATGA 900
301 LeuAspArgTrpGlyArgThrAlaLeuIleLeuAlaValaCysCysGlySe 317
|||||
901 CTGGATGATATGGAAGAGACTGCTCATATCTTGGCTGATATGTTGGATC 950
317 rAlaSerIleValSerLeuLeuLeuGlnHisAsnIleAspValSerSerg 334
|||||
951 AGCAAGTATAGTCAGCTTCTTACTTACAGCAAAATATGATGATATCTTCTC 1000
334 LysAspLeuSerGlyGlnThrAlaArgGlyLysTrpAlaValSerSerHis 350
|||||
1001 AGATTCATCTGGACACAGCGCCAGAGATATGCTTTCTTACATCAT 1050
351 HisValIleCysGlnLeuLeuSerAspTrpLysGlnLysGlnMetLeuL 367
|||||
1051 CATGTATTTGGCCAGTACTTCTTGACTACAAAGAAAAAGATGACTAA 1100
367 sIleSerSerGlyLysAsnSerAsnProGluAsnValSerArgThrArgAsn 384
|||||
1101 AATCTCTTCGAAACAGCAATCCAGAAATGTCTCAAGAACCAATA 1150
384 ys 384
||
1151 AA 1152

seq_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT:AA167211
seq_documentation_block:
ID AA167211 standard; CDNA: 1155 BP.
XX
AC AA167211;
XX
DT 11-FEB-2002 (first entry)
XX
DE B305D isoform C splice variant 1 encoding CDNA.
XX
KW Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
cancer; B305D; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 1..1155
FT /tag= a
FT /product= "B305D isoform C splice variant"
XX
PN MO200175171-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-US10631.
XX
PR 03-APR-2000; 2000US-194241P.
PR 20-JUL-2000; 2000US-219862P.
PR 27-JUL-2000; 2000US-221300P.
PR 18-DEC-2000; 2000US-256592P.
XX
PA (CORI-) CORIXA CORP.

```

XX Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;  
PI WPI; 2001-626449/72.  
XX P-PSDB; AAG65976.  
XX  
XX Identifying tissue (tumour)-specific polynucleotides overexpressed in  
PI tissue of interest as compared to control tissue, for detecting cancer  
PI cells in patient, comprises DNA microarray analysis or quantitative  
PI polymerase chain reaction -

PS Claim 4; Page 93-94; 127pp; English.

XX  
XX The invention relates to identifying tissue-specific polynucleotides (P)  
CC that involves performing a genetic subtraction to identify pool of (P)  
CC from tissue of interest (TI), performing DNA microarray analysis to  
CC identify first subset of polynucleotides (SP1) at least 2-fold over  
CC expressed in TI, and performing quantitative polymerase chain reaction  
CC (PCR) analysis on SP1 to identify second subset of (P). The method is  
CC useful for determining the presence or absence of a cancer cell in a  
CC patient, monitoring the progression of cancer in a patient using a  
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,  
CC urine or a tumour biopsy sample. The methods are useful for determining  
CC the presence or absence of or monitoring progression of prostate, breast,  
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,  
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present  
CC sequence represents a cDNA encoding a B305D isoform C splice variant.

XX Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other:

alignment\_scores:

Quality: 2064.00 Length: 384  
Ratio: 5.375 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-810-936-304 x AAI67211 ..

Align seg 1/1 to: AAI67211 from: 1 to: 1155

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1 ATGGGGTGGAGTTGATTCATGCGCGCTCTTCTGTGAGAGAGCC 50  
17 oPhedGlyLeuArgSerLysMetGlyLysTrpCysCysArgCysPheProC 34  
51 ATTGGCTCTCAGAGCAAGATGGCAGATGCTGCTGCCCTTCCCT 100  
34 YsCysArgGluSerGlyLysSerAsnValGlyThrSerGlyAspHisAsp 50  
101 GCTGCGAGGAGAGCGGCAAGACACTGGGCACTTCTGAGAGCCAGAC 150  
51 AspSerAlaMetLysThrLeuArgSerLysMetGlyLysTrpCysArgH 67  
151 GACTCTGCTATGAGACACTCAGAGCAAGATGAGCAAGTGTGCCGCA 200  
67 sCysPheProCysCysArgGlySerGlyLysSerAsnValGlyAlaSerG 84  
201 CTGCTTCCCTGCTGCAAGGGAGAGTGGCAGACAACTGGGCGCTTCTG 250  
84 LysPheHisAspAspSerAlaMetLysThrLeuArgAsnLysMetGlyLys 100  
251 GAGACCAAGACGACTGTATGAAACACTCAGGAACAAGATGGGCAAG 300  
101 TrpCysCysHisCysPheProCysCysArgGlySerGlyLysSerLys 117  
301 TGGTGTCTCCACTGCTTCCCTGTGAGGGGAGAGCGGCAAGAGG 350  
117 IGIAlaTrpGlyAspTrpAspAspSerAlaPheMetGluProArgTyrH 134  
351 GGGGCGCTGGGAGACTAGCATGACAGTGCCTTCATGAGACCCAGGTACC 400

134 tSValArgGlyGluAspLeuAspLysLeuHisArgAlaAlaTrpTrpGly 150  
401 ACGTCGCTGGAGAGATCTGGACAAAGCTCCACAGAGCTGCTGGTGGGCT 450  
151 LysValProArgTrpLysAspLeuIleValMetLeuArgAspPheAspValAs 167  
451 AAAGTCCCAAGAAAGGATCTCATCTGCTACAGCTCAGGAGCACTGAGTAA 500  
167 nLysLysAspLysGlnLysArgTrpAlaLeuHisLysLeuAlaSerAlaAng 184  
501 CAAGAAAGACCAAGCAAAAGAGAGCTGCTACATCTGGCGCTTGGCAATG 550  
184 LysAsnSerGluValValLysLeuLeuLeuAspArgCysGlnLeuAsn 200  
551 GGAATTCAGAAAGTAAAGAACTCTGCTGAGACGACGATGTCACACTTAA 600  
201 ValLeuAspAsnLysLysArgTrpAlaLeuIleLysAlaValGlnCysG 217  
601 GTCTTGTACACAAAGAAAGAGACGCTGATTAAGGCGGTACATGCGCA 650  
217 nGluAspGluCysAlaLeuMetLeuGluHisGlyThrAspProAsn 234  
651 GGAAGATGAATGTCGCTTAATGTTGCTGGAACATGCGCATGCCAATA 700  
234 lProAspArgLysTrpGlyAsnThrThrLeuHisTyrAlaAlaTyrAsnGlu 250  
701 TTCACAGTAGATGGAATATACACTCTGCACTAGCGTATCTATATGAA 750  
251 AspLysLeuMetAlaLysAlaLeuLeuLeuLysGlyAlaAspIleGluSe 267  
751 GATAAATTAATGGCCAAAGACACTGCTTAATGATGATGATGATGATG 800  
267 rLysAsnLysHisGlyLeuThrProLeuLeuLeuGlyValHisGluGln 284  
801 AAAAACAAGCATGGCTCTACACACACTGTACTGTGTTGACTGACGAAA 850  
284 YsGlnGlnValValLysPheLeuIleLysLysLysAlaAsnLeuAsnAla 300  
851 AACGCAAGTCCTGAAATTTTAAATCAAGAAAAAGCGAATTTTAAATGCA 900  
301 LeuAspArgTrpGlyArgTrpAlaLeuIleLeuAlaValCysCysGlySe 317  
901 CTGATATGATATGGAAGAGACTGCTCATACCTTGCTGATGTGTTGGAATC 950  
317 rAlaSerIleValSerLeuLeuLeuGluGlnAsnIleAspValSerSerg 334  
951 AGCAAGATATGCTCAGCCTTCTACTTACGCAAAATATGATGATCTTCTC 1000  
334 lAspLeuSerGlyGlnThrAlaArgLysGlyLysAlaValSerSerHis 350  
1001 AAGATCTATCTGGACAGAGCGGCAAGAGATGCTGTTCTGATCATCAT 1050  
351 HisValIleCysGlnLeuLeuSerAspTrpLysGluLysGlnMetLeuLys 367  
1051 CATGTAAATTTGGCAGATTACTTCTGACTACAAAGAAACAAATCTCTAAA 1100  
367 sIleSerSerGluAsnSerAsnProGluAsnValSerArgTrpArgAsn 384  
1101 AATCTCTTTCGAAAAACGCAATCCAGAAATGTCCTCAAGAACACAGAAATA 1150  
384 Ys 384  
1151 AA 1152

seq\_name: /STD/SI/gcgdata/hold-geneseg/genesegn-emb1/NA2001A.DAT:AA563807

seq\_documentation\_block:

ID AA563807 Standard; cDNA, 1155 BP.

XX

AC AA563807;

XX

DT 29-JAN-2002 (first entry)

XX



1001 AAGATCTATCTGGACAGCGCCAGAGATGCTGTTCTAGTCATCAT 1050  
351 HisVal11ecySgInleuSerAspTyrLysGluLysGlnMetLeuLys 367  
1051 CAGGTAAATTTGCCAGTACTTCTGACTACAAAGAAACACAGTCTAAA 1100  
367 s1leSerSerGluAsnSerAsnProGluAsnValSerArgThrArgAsnL 384  
1101 AATCTCTTGAAACAGCAATCCAGMAAATGTCCTCAAGACCAAGAAATA 1150  
384 ys 384  
1151 AA 1152

seq\_name: /STD1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAH93714

seq\_documentation\_block:

ID AAH93714 standard; cDNA; 1155 BP.

AAH93714:

04-OCT-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #8.

Human: prostate cancer; prostate-specific; diagnosis; vaccine;

cytostatic; gene therapy; metastasis; ss.

Homo sapiens.

MO200151633-A2.

19-JUL-2001.

16-JAN-2001: 2001WO-0501574.

14-JAN-2000: 2000US-0483672.

(COR1-) COR1XA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;

WPI; 2001-425873/45.

New polynucleotide encoding a prostate-specific protein, for

diagnosis, monitoring and treating prostate cancer in a patient and

for use in vaccines -

Claim 1, Page 347; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode  
prostate-specific proteins (II). (I) and (II) have cytostatic activity,  
and can be used in vaccine production and gene therapy. (I), (II),  
antibodies to (II), fusion proteins comprising (II), and isolated  
T cells prepared using (I) or (II) are used to treat cancer in a patient.  
(I) and the antibodies are also used in the detection of cancer in a  
patient. The cancer that is diagnosed or treated is particularly  
prostate cancer. (I) and (II) can be used in vaccines. The antibodies or  
(I) can be used for monitoring the progression of cancer in a patient.  
(I) and (II) can also be used to improve diagnostic and therapeutic  
methods for prostate cancer. They can indicate the level of metastasis  
as well as the prostate volume. AAH93714 to AAH93944 and AAM01115 to  
CC AAM01318 represent polynucleotide and amino acid sequences used in the  
embodiment of the present invention.

Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

alignment\_scores:

Quality: 2064.00

Ratio: 5.375

Length: 384

Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-810-936-304 x AAH93714 ..

Align seg 1/1 to: AAH93714 from: 1 to: 1155

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1 ATGGTGTTGAGGTTGATTCATGCGCGGCTGCTCTTCGTGAAGAACCC 50  
17 ophEGiLyeuArgSerLysMetGlyLysTrpCysArgCysPheProC 34  
51 ATTTGGTCTCAGAGCAAGATGGGCAAGGTGTCGCTTCCTCCCT 100  
34 yscysArgGluSerGlyLysSerAsnValGlyThrSerGlyAspHisAsp 50  
101 GCTGCAGGAGAGCGGCAAGACCAAGTGGGCACTTCTGGAGACCAGAC 150  
51 AspSerAlaMetLysThrLeuArgSerLysMetGlyLysTrpCysArgH 67  
151 GACTCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCCA 200  
67 scysPheProCysArgGlySerGlyLysSerAsnValGlyAlaSerG 84  
201 CTGCTTCCTCCCTGCTGCAGGGGAGTGGCAAGAGCAACGTGGCGCTTCTG 250  
84 lysAspHisAspSerAlaMetLysThrLeuArgAsnLysMetGlyLys 100  
251 GAGACCAAGCAAGCTCTGATGAGACACTCAGGAAACAGATGGGCAAG 300  
101 TrpCysArgHisCysPheProCysArgGlySerGlyLysSerLysVal 117  
301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGT 350  
117 lGlyAlaTrpGlyAspTyrAspAspSerAlaPheMetGluProArgTyrH 134  
351 GGGCGCTGGGAGACTACATGACAGTCCCTTCATGAGCGCCAGGTAC 400  
134 lValAlaArgGluGluAspLysLysLysLysLysLysLysLysLysLys 150  
401 ACGTCCGTGGAGAGATCTGGACAGCTCCACAGAGCTCCGTGGGGGT 450  
151 LysValProArgLysAspLeuIleValMetLeuArgAspThrAspValAs 167  
451 AAAGTCCCGCAGAAAGATCTCATGCTCAGGCGACACTGACGTGAA 500  
167 nLysLysAspLysGlnLysArgThrAlaLeuHisLeuLysSerAlaAsn 184  
501 CAGAGAGCAAGCAAGAGAGCTCTACATGTGGCTGGCTGGCAATG 550  
184 lAsnSerGluValLysLeuLeuLeuAspArgCysGlnLeuAsn 200  
551 GGAATTCAGAAATGTAAGAACTCTGCTGACAGCAAGATGTCACACTAAT 600  
201 ValLeuAspAsnLysLysArgThrAlaLeuIleLysAlaValGlnCysG 217  
601 GTCCTTGACACAAAGAGAGAGCTGTGATTAAGGCCGTTCATATGCCA 650  
217 nGluAspGluCysAlaLeuMetLeuGlnIleGlyThrAspProAsn 234  
651 GGAAGATGAATGTGCGTTAATGTGCTGGAACATGGACATGATCCAAATA 700  
234 lProAspArgLysLysLysLysLysLysLysLysLysLysLysLysLys 250  
701 TTCAGATGAGTGTGAATACCACTGTGCACTAGCCTATCATTAATGAA 750  
251 AspLysLeuMetAlaLysAlaLeuLeuLeuTyrGlyAlaAspLysG 267  
751 GATAAATTAATGSCCAAGACACTGCTTATATGAGTGAATGCAATC 800  
267 LysAsnLysHisGlyLeuThrProLeuLeuLeuLysLysGlnL 284

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801 AAAAACAAGCATGGCTCAACACACTTACTTGGTGTACATGAGCAA 850
284 ysgingivalValylsphenuleuileuLysLysAlaAsnleuAsnAla 300
851 AACGCAAGTCGGAATATTTAAATCAAAAAAGCAATTTAAATGCA 900
301 LeuAspArgTyrGlyArgThrAlaLeuileuAlaValCysCysGlySe 317
901 CTGATATGATATGAGAGAGACTGCTCTCATCTGCTGTATGTGTGATC 950
317 TalasertilleValserleuLeuLeuGlnAsnIleAspValSerSerg 334
951 AGCAAGATAGTCAGCCCTTCTACTGAGCAAAATATGATGATCTCTC 1000
334 InAspLeuSerGlyGlnThrAlaArgLutYrAlaValSerSerHisH 350
1001 AAGATCTATCTGGACAGACGCCAGAGACTATGCTTTCATGATCAT 1050
351 HisValIleCysGlnLeuLeuSerAspTyrLysGlyLysGlnMetLeu 367
1051 CATGTAAATTTGCCAGTTACTTCTGTACTCAAAAGAAAAACGATGCT 1100
367 sIleSerSergLysAsnSerAsnProGlnAsnValSerArgThrArg 384
1101 AATCTCTTCAAAACAGCAATGCAGAAATGTCAGAGAACCAATA 1150
384 ys 384
1151 AA 1152
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seq_documentation_block:
ID AAH85028 standard; cDNA; 1155 BP.
XX
AC AAH85028;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #8.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KM chromosome 22q11.2; prostate-specific protein; chromosome 1;
KN prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30904.
XX
PR 12-NOV-1999; 9905-0439313.
PR 18-NOV-1999; 9905-0443686.
XX
PA (COR1-) COR1XA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YMW, Wang A;
XX
DR WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
PS Claim 31: Page 246-247; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (M1) encoding (P1). (P1) and
CC (M1) have cytostatic activity and can be used in vaccine production.
```

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CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
Alignment_scores:
Quality: 2064.00 Length: 384
Ratio: 5.375 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-810-936-304 x AAH85028 ..
Align seg 1/1 to: AAH85028 from: 1 to: 1155
1 MetValAlaGluValAspSerMetProAlaIleSerValLysLysPr 17
1 ATGGTGGTTGAGGTTGATTCATGCGCGCTCTTCTGTGAAGAAAGCC 50
17 OPheGlyLeuArgSerLysMetGlyLysTyrPcysCysArgCysPheProC 34
51 APTTGGTCTCAGAGCAAGATGGCGCAAGTGGTCCCTGCTTCCCT 100
34 yScyArGluSerGlyLysSerAsnValGlyThrSergLysAspHisAsp 50
101 GCTGACAGGAGAGCGGCAAGACAGCACTGGGCACTTCTGGAGACCAAC 150
51 AspSerAlaMetLysThrLeuArgSerLysMetGlyLysTyrPcysArgH 67
151 GACTCTGCTATGAAGACATCAGAGCAAGATGGCAAGTGGTGGCCGCA 200
67 sCysPheProCysCysArgGlySergLysSerAsnValGlyAlaSerg 84
201 CTGCTCCCTGCTGCGAGGGAGTGCAGAGCAAGCGGCGCTTCTG 250
84 LysAspHisAspAspSerAlaMetLysThrLeuArgAsnLysMetLys 100
251 GAGACACGACGACTGCTATGACACACTCAGGACACAGATGGGCAAG 300
101 TrpCysCysHisCysPheProCysCysArgGlySergLysSerLysVa 117
301 TGGTGTGCTGCCACTGCTTCCCTGCTGCAAGGGAGGCGCAAGCAAGT 350
117 LGlyAlaThrGlyAspTyrAspAspSerAlaPheMetGluProArgTyrH 134
351 GGGCGCTTGGGGACTACATGATGACATGCTCTCATGGAGCCCAAGTAC 400
134 IsValArgGlyGluAspLeuAspLysLeuHisArgAlaIleArgTyrP 150
401 ACGTCCGTGGAGAGATCTGACACACTCCACAGACTCCCTGCTGGCG 450
151 LysValProArgLysAspLeuIleValMetLeuArgAspThrAspValAs 167
451 AAGTCCCGCAAGAGATCTCATGCTGATGCTCAGGAGACATGAGAGTAA 500
167 nLysLysAspLysGlnLysArgThrAlaLeuHisLeuAlaSerAlaAsn 184
501 CAAGAGAGCAAGCAAAAGAGACTGCTCTACATCTGGCTCTGCCAATG 550
184 LysAsnSergLysValLysLeuLeuLeuAspArgArgGlyGlnLeuSn 200
551 GGAATTCAGAGTGTAAAACTCTCTGTGACAGAGAGATGTAACCTTAAT 600
201 ValLeuAspAsnLysLysArgThrAlaLeuIleLysAlaValGlnCysG 217
601 GTCCTTGACACAAAGAGAGAGAGCTCTGATTAAGGCCGTAACTATGCCA 650
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217 nGIuAspGIuCysAlaLeuMeLeuLeuGluHisGlyThrAspProAsnI 234
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DR MP1: 2001-245062/25.
DR P-PSDB: AAB74815.
XX Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
PT Claim 50; Page 231-232; 276pp; English.
XX
XX The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

alignment_scores:
    Quality: 2064.00      Length: 384
    Ratio: 5.375          Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment block:
US-09-810-936-304 x AAH02779 ..

Align seg 1/1 to: AAH02779 from: 1 to: 1155

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151 GACTTCGCTATGAAACACTCAAGACCAAGATGGGCAAGTGGCGGCA 200
67 sCysPheProCysCysArgGlySerGlyLysSerAsnValGlyAlaSerG 84
201 CTGCTCCCTCCCTGCTGCGAGGGGAGTGGCAAGCAAGTGGGCGCTCTG 250
84 LysAsnHisAspSerAlaMetLysThrLeuArgAsnLysMetGlyLys 100
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301 TGGTGGTGGCCACATGCTTCCCTGCTGAGGGAGCGCAAGCAAGAGT 350
117 LysValAlaTrpGlyLysTrpAspArgSerLysLysMetGlyProAlaGlyH 134
351 GGGGCGTTGGGAGACTAGATGACAGTGGCTTCCAGGAGCCAGGAGTACC 400
134 LysValArgGlyLysLysLysLysLysLysLysLysLysLysLysLys 150
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151 LysValProArgLysAspLeuLeuValMetLeuAlaGlyAspThrAspValAs 167

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451 AAAGTCCCGAAGAAAGATCTCATGCTCATGCTCAGGACACTGACGTGCA 500
167 nLysLysAspLysGlnLysArgThrAlaLeuHisLeuAlaSerAlaSer 184
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551 GGAATTCAGAAAGTAAAGTAACTCTGCTGACAGACGATGTCACACTTAT 600
201 ValLeuAspAsnLysLysArgThrAlaLeuIleLysAlaValGlnCysG 217
601 GTCCCTTACAAACAAAGAGAGACGCTCGATTAAGGCGGTACATGCA 650
217 nG1AspG1ucysAlaLeuMetLeuGlnHisGlyThrAspProAsn 234
651 GGAAGATGAATGTGCGTTATGTGCTGACATGCGACTGATCCAAATA 700
234 LeproAspGluTyrGlyAsnThrThrLeuHisTyrAlaIleTyrAsnG 250
701 TTCAGATGAGTATGGAATATCACCTCTGCTACGCTATCATATATATA 750
251 AspLysLeuMetAlaLysAlaLeuLeuLeuTyrGlyAlaAspIleGlu 267
751 GATAAATTAAATGGCCAAAGACACTGCTTATATAGTGTGATATGATG 800
267 rLysAsnLysHisGlyLeuThrProLeuLeuGlnLysValHisGlnGln 284
801 AAAAACAAGATGCGCTCACACACTGTTACTGGTGACTGAGCAAA 850
284 ysgInglInValValLysPheLeuIleLysLysAlaAsnLeuAsnAla 300
851 AACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCGAATTAAATCA 900
302 LeuAspArgTyrGlyArgThrAlaLeuIleLeuAlaValCysGlySe 317
901 CTGATGATATATGCAAGACACTGCTCATATCTTGCTGATGTGTGGAT 950
317 rAlaSerIleValSerLeuLeuLeuGlnGlnAsnIleAspValSerSer 334
951 AGCAAGATATAGTACGCCCTTCTACTTACGCAAAATATGTGATCTTC 1000
334 LAspLeuSerGlnThrAlaArgGluTyrAlaValSerSerHisHis 350
1001 AAGATCTATCTGACACAGCGCCAGAGATGCTTTCTTGTATCATCAT 1050
351 HisValIleCysGlnLeuLeuSerAspTyrLysGlnLysGlnMetLeu 367
1051 CATGTAATTTGCCAGTTACTTTCTGACTACAAAGAAAAACAGATCTAA 1100
367 sIleSerSerGlnAsnSerAsnProGlnAsnValSerArgThrArgAsn 384
1101 AATGCTCTCTGAAGACGAAATCCAGAAATGTCTCAAGACCAAAATA 1150
384 ys 384
1151 AA 1152
seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT: AAS9857
seq_documentation_block:
ID AAS9857 standard; cdna; 1155 BP.
XX
XX AAS9857;
XX
XX 12-MAR-2002 (first entry)
XX
XX Breast tumour-specific DNA B1Aq1 splice variant B1C-15.
XX
XX Human: breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
XX
XX tumour; vaccine; immunogenic.
XX
XX Homo sapiens.

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XX
XX PN WO200190152-A2.
XX
XX PD 29-NOV-2001.
XX
XX PF 22-MAY-2001; 2001WO-US16776.
XX
XX PR 24-MAY-2000; 2000US-0577505.
XX PR 08-JUN-2000; 2000US-0590583.
XX PR 26-OCT-2000; 2000US-0699293.
XX PR 16-MAR-2001; 2001US-0810936.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
XX PI Wang A, Skeiky YAM, Harlocker SL, Day CH;
XX
XX DR WPI: 2002-089919/12.
XX DR P-PDB: AAU74377.
XX
XX PT New breast tumour proteins and polynucleotides encoding them, useful for
XX PT treating and/or preventing cancer, particularly breast cancer, and for
XX PT eliciting humoral and/or cellular immune response
XX
XX PS Claim 1; Page 223; 245pp; English.
XX
XX CC The invention relates to novel breast tumour polynucleotides and
XX CC polypeptides. The polypeptides and polynucleotides are useful in
XX CC pharmaceutical compositions for treating and/or preventing cancer,
XX CC particularly breast cancer, and for eliciting an immune response,
XX CC may be used as probes or primers for nucleic acid hybridisation, in the
XX CC design and preparation of ribozyme molecules for inhibiting expression of
XX CC tumour polypeptides and proteins, and in recombinant DNA molecules to
XX CC direct expression of a polypeptide in host cells. AAS9570-AAS9888
XX CC represent novel human breast cancer protein coding sequences and
XX CC PCR primers of the invention.
XX
XX SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
XX
XX alignment_scores:
XX          Quality: 2064.00      Length: 384
XX          Ratio: 5.375          Gaps: 0
XX          Percent Similarity: 100.000      Percent Identity: 100.000
XX
XX alignment_block:
XX          US-09-810-936-304 x AAS9857 ..
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XX Align seg 1/1 to: AAS9857 from: 1 to: 1155
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XX 1 ATGGTGGTGAAGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAGCC 50
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XX 17 oPheGlyLeuArgSerLysMetGlyLysTyrCysArgCysPheProc 34
XX |||||||
XX 51 ATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCTGCTTCTCCCT 100
XX
XX 34 yscysArgGlnSerGlyLysSerAsnValGlyThrSerGlyAspHisasp 50
XX |||||||
XX 101 GCTGCAAGGAGACGCGCAAGACGACGTCGACCTTCTGGAGACACGAC 150
XX
XX 51 AspSerAlaMetLysThrLeuArgSerLysMetGlyLysTyrCysArgH 67
XX |||||||
XX 151 GACTCTGCTATGAAGACACTCAAGACCAAGATGGGCAAGTGGTCCGCA 200
XX
XX 67 scysPheProCysArgGlySerGlyLysSerAsnValGlyAlaSerG 84
XX |||||||
XX 201 CTGCTTCCCTGCTGCGAGGGAGCTGGCAAGACGACGCTGCTCTG 250
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XX 84 LysAspHisAspAspSerAlaMetLysThrLeuArgAsnLysMetGlyLys 100
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167	nLysLysAspLysGlnLysArgTrpAlaLeuHISLeuAlaSerAlaAspG	184
501	CAGAAGGACAAAGCAAAAGAGAGCTGCTTACATCTAGTGGCTCTGGCCATG	550
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601	GTCCTTTGACAAACAAAGAGAGACAGCTGTGATTAAGGCCGTACATGCCA	650
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751	GATTAATTAATATGGCCAAAGCACTGCTTTAATATGATGCTGTATACGAATC	800
267	TrysAsnLysHISGlyLeuTrpProLeuLeuLeuGlyValHISGluGln	284
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901	CGGGAATGATATGGAAGGACGTGCTCTCATACTGGTGTATCTGTGGATGC	950
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334	LasPheLysSerGlyGlnThrAlaArgGlyTyrAlaValaSerSerHISHis	350
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1051	CATGTATATTTGGCACTTACTTCTTACTACACAAAGAAAAACAGATGCTTAA	1100
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ID   AA599869 standard; DNA; 1590 BP.
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AC	AAS99869;
XX	
DT	12-MAR-2002 (first entry)

DE Breast tumour-specific gene B305D fusion construct.

AA  
KW  
KW  
Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;  
tumour; vaccine; immunogenic.

OS Homo sapiens.

PN WO200190152-A2.

PD 29-NOV-2001.

PF 22-MAY-2001; 2001WO-US16776.

PR 24-MAY-2000; 2000US-0577505

PR 26-OCT-2000; 2000US-0699295

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PI Wang A, Skelky YAW, Hartloof

DR WPI: 2002-089919/12

PT	New breast tumour p
DT	4.5 ± 0.5 and 4.0 ± 0.5

PI electing humoral an

Example 8; Page 233

the invention relates to

pharmaceutical compo

particularly numerals.

design and preparation

CC direct expression of

CC PCR primers of the

sequence 1390 bp; 4.

21 January 2007

Quality: 200  
Rating: 5

Percent Stimulability: 100

adLynmenc\_block;  
TTC=08-810-936-304 x AAC

Alien and 1/1 to: AASC9

1 Mat+va]va]C]u]va]

A36 AAAAAAAAAA

17 OBJECT: TOWNSHIP RECORDS

[illegible]

34 yscysarqgluserglylyssersanvalglythrserglyaspHisasp 50  
 |||||  
 536 GCTGCAGGAGGAGCGGCAAGACAGTGGCAGCTTCTGGAGACAGAC 565  
 51 AspSerAlaMetLysThrLeuArgSerLysMetGlyLysTrpCysAlaGHI 67  
 |||||  
 586 GACTGTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGTCTCCGCCA 635  
 67 sCysPheProCysArgGlySerGlyLysSerAsnValGlyAlaSerG 84  
 |||||  
 636 CTGCTTCCCTGCTGCGAGGGGAGTGGCAAGACACGTGGGCCCTCTG 685  
 84 LysPheHisAspSerAlaMetLysThrLeuArgAsnLysMetGlyLys 100  
 |||||  
 686 GAGACCCAGCAGACTCTGCTATGAGACACTCAGGAACAAATATGGCAG 735  
 101 TrpCysGlyHisCysPheProCysArgGlySerGlyLysSerLysVal 117  
 |||||  
 736 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765  
 117 LGLYALATrPGLYAspTrpAspAspSerAlaPheMetGluProArgTrpH 134  
 |||||  
 786 GGGGGCTGGGGGAGACTACGATGACAGTCCCTCATGGAGCCAGGTACC 835  
 134 LsValArgGlyGluAspLeuAspLysLeuHisArgAlaAlaTrpTrpGly 150  
 |||||  
 836 ACGTCCGTGGAGAAAGATCTGGACAAAGCTCCACAGAGCTGCTGGTGG 885  
 151 LysValProArgLysAspLeuLeuValMetLeuArgAspThrAspValAs 167  
 |||||  
 886 AAAGTCCCGAGAAAGATCTCATGCTCATGCTCATGAGGACACTGACGTGA 935  
 167 nLysLysAspLysGlnLysArgThrAlaLeuHisLeuAlaSerLysAsnG 184  
 |||||  
 936 CAGAGAGGACAGCAAAAGAGGAGCTGCTACATGCTGCTGCTGCTGCTG 985  
 184 LysAsnSerGluValValLysLeuLeuLeuAspArgArgCysGlnLeuAsn 200  
 |||||  
 986 GGAATTCAGAAAGTAACTCTGCTGAGACAGACGATGCAACTTAAT 1035  
 201 ValLeuAspAsnLysLysArgThrAlaLeuLeuLysAlaValGlnCysG 217  
 |||||  
 1036 GTCTTACACACAAAGAGAGAGCTGCTGATTAAGGCCGCTACATGCA 1085  
 217 nGluAspGluCysAlaLeuMetLeuLeuGlnHisGlyThrAspProAsnI 234  
 |||||  
 1086 GGAAGATGAATGCGCTTAATGTTGCTGGAACATGGCAGTCAATAA 1135  
 234 LeProAspGluLysArgLysAsnThrThrLeuHisTrpAlaIleTrpAsnGlu 250  
 |||||  
 1136 TTCCAGATGAGTATGGAATACCACTCTGCACTACGCTATCTATATGAA 1185  
 251 AspLysLeuMetAlaLysAlaLeuLeuLeuTyrglyAlaAspIleGluSe 267  
 |||||  
 1186 GATTAATTAATGGCCAAAGCACTGCTTAATGCTGCTGATATCGAATC 1235  
 267 rLysAsnLysHisGlyLeuThrProLeuLeuLeuGlnLysValHisGlnGlu 284  
 |||||  
 1236 AAAAANAACATGAGCTCAGACACACACTGTTACTTGTCTATATAGCAA 1285  
 284 ysgGlnGlnValValLysPheLeuLeuLysLysLysAlaAsnLeuAsnAla 300  
 |||||  
 1286 AACGGCAAGTCGTGAATTTTAATCAAAAAAAAAGCAAAATTTAAATGA 1335  
 301 LeuAspArgTrpGlyArgThrAlaLeuLeuLeuAlaValCysCysGlySe 317  
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 1336 CTGATATGATATGAGAGAGCTGCTCATCTTGTCTGATGTGTGGATC 1385  
 317 rAlaSerIleValSerLeuLeuLeuGlnGlnAsnIleAspValSerSerG 334  
 |||||  
 1386 AGCAAGATATGATGACGCTTCTACTTGAAGCAAAATATGATGATCTTCTC 1435

334 LAspLeuSerGlyGlnThrAlaArgGluTrpAlaValSerSerHisHis 350  
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 1436 AAGATCTATCTGACAGACAGCGCAAGATGCTGTTCTTACGATCAATC 1485  
 351 HisValIleCysGlnLeuLeuSerAspTrpLysGlnLysGlnMetLeuTy 367  
 |||||  
 1486 CAGTGTATTTGCCAGTTACTTCTCTGATACAAAGAAAAAGATGCTAA 1535  
 367 sLleSerSerGluAsnSerAsnProGluAsnValSerArgThrArgAsnL 384  
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 1536 AATCTCTTCTGAAACAGCAATTCAGAAAAATGCTCAAGAACAGAAATA 1585  
 384 Ys 384  
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 seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:AA599872  
 seq\_documentation\_block:  
 ID AA599872 standard; DNA; 1155 BP.  
 XX  
 AC AA599872;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Breast tumour-specific gene B305D homologue #2.  
 XX  
 KW Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;  
 KW tumour; vaccine; immunogenic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200190152-A2.  
 XX  
 PD 29-NOV-2001.  
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 PE 22-MAY-2001; 2001WO-US16776.  
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 PF 24-MAY-2000; 2000US-0577505.  
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 PR 08-JUN-2000; 2000US-0590583.  
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 PR 26-OCT-2000; 2000US-0699295.  
 XX  
 PR 16-MAR-2001; 2001US-0810936.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;  
 PI Wang A, Skeiky YAW, Harlocker SL, Day CH;  
 DR WPI; 2002-089919/12.  
 DR P-PSDB; AAU74390.  
 XX  
 PT New breast tumour proteins and polynucleotides encoding them, useful for  
 PT treating and/or preventing cancer, particularly breast cancer, and for  
 PT eliciting humoral and/or cellular immune response  
 XX  
 PS Claim 1; Page 239; 245pp; English.  
 XX  
 CC The invention relates to novel breast tumour polynucleotides and  
 CC polypeptides. The polypeptides and polynucleotides are useful in  
 CC pharmaceutical compositions for treating and/or preventing cancer,  
 CC particularly breast cancer, and for eliciting an immune response,  
 CC particularly humoral and/or cellular immune response. The polynucleotides  
 CC may be used as probes or primers for nucleic acid hybridisation, in the  
 CC design and preparation of ribozyme molecules for inhibiting expression of  
 CC tumour polypeptides and proteins, and in recombinant DNA molecules to  
 CC direct expression of a polypeptide in host cells. AA599570-AA599888  
 CC represent novel human breast cancer protein coding sequences and  
 CC PCR primers of the invention.  
 XX  
 SQ Sequence 1155 BP; 346 A; 253 C; 296 G; 260 T; 0 other;

alignment\_scores:

Quality: 2054.00 Length: 384  
 Ratio: 5.349 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 99.479

alignment\_block:  
 US-09-810-936-304 x AAS99872 ..

Align seg 1/1 to: AAS99872 from: 1 to: 1155

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1 MetValValAlGluValAspSerMetProAlaAlaSerValIlyLysIleP 17
  |||
1 ATGGTGGTTGAGGTGATTCATGCCGGCTGCTCTCTCTGTAAGAAAGCC 50
17 oPhEgIleuAArgSerIyMetGlyIleTPCyScyArqCySphProc 34
  |||
51 ATTTGGTCTCAGAGCAAGATGGCAGTGGTGGTGGTGGTGGTGGTGGTGG 100
34 yScyArqGluSerGlyIleSerAsnValGlyThrSerGlyAspHisAsp 50
  |||
101 GCTGCAGGGAGAGCGGCAAGCAAGCTGGCGACTCTGGAGACCGAGAC 150
51 AspSerAlaMetIyThrIleuAArgSerIyMetGlyIleTPCyScyArq 67
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67 sCySphProcCyScyArqGlySerGlyIleSerAsnValGlyIleAsp 84
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201 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 250
84 IyAspHisAspAspSerAlaMetIyThrIleuAArgAsnIyMetGlyLys 100
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251 GAGACCGACGACACTCTGCTATGAGACACTCAGAGCAAGATGGGCAAG 300
101 TrpCyScyHisIleScySphProcCyScyArqGlySerGlyIleSerLys 117
  |||
301 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 350
117 IGIValATrPGlyAspTyrAspAspSerAlaPheMetGluProArgTyr 134
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134 IValAlaArgGlyIleAspIleuAspIyLysIleAsnValAlaAlaTrp 150
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401 ACGTCCCTGGAGAAATCTGGACAAGCTCCACAGAGCTGGTGGGGGT 450
151 LysValProArgIyAspIleuIleValMetIleuAArgAspThrAspVal 167
  |||
451 AAGTCCCGCAAGAAAGATCTCATGCTCATGCTCAGGGACACTGAGCT 500
167 nIyLysIyAspIyGlnIyAsnIleAlaIleuHisIleuAlaSerAla 184
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501 CAAGCAGACAGCAAGAAAGAGAGCTCTCTACATCTGGCTCTGCCAAT 550
184 IyAsnSerGluValIleLysIleuIleuAspArgCysGlnIleuAsn 200
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551 GGAATTCAGAAAGTAAATAAATCTCTGAGACAGACAGATGCACTTAAT 600
201 ValIleuAspAsnIyLysArgThrAlaIleuIleLysAlaValGlnCys 217
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601 GTCTTGTGACAAACAAAGAGAGAGCTCTGATTAAGGCCGTAACAAT 650
217 nGluAspGluCysAlaIleuMetIleuGlnHisGlyThrAspProAsn 234
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651 GGAAGATGATGTGCTTAATGTGTGTGACATGACATGCAATCAATA 700
234 IeProAspGluIyGlyAsnThrIleuHisIyAlaIleTyrAsnGlu 250
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701 TTCAGATGAGTAAATACACACTCTCAGTACATATATATATATATA 750
251 AspIyLysIleuMetAlaLysAlaIleuIleuIyGlyAlaAspIleGlu 267
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751 GATTAATTAATGGCAAGACACTGCTTATATATGTGTGTGTGTGTAT 800

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267 IlyAsnIyHisGlyIleuThrProIleuIleuGlyValIleGlnGlnI 284
  |||
801 AAAAACACAGCATGGCTCACACACTGTACTTGTGTGTGTGTGTGTGT 850
284 ySGInGlnValIlySphIleuIleLysIyLysAlaAsnIleuAsnAla 300
  |||
851 AACGCAAGTCGTGAATAATTTAATTAAGAAAAAGCCGAAATTTAAAT 900
301 IeAspArgTyrGlyArgThrAlaIleuIleLysAlaValCysGlyLys 317
  |||
901 CTGGATAGATATGAGAGAGACTGCTCTCATACTTGTGTGTGTGTGTGT 950
317 rAlaSerIleValSerIleuIleuGlnIleuAsnIleAspValSerS 334
  |||
951 AGCAAGATATGTCAGCTTCTACTTACGCAAAATATGATGATCTCTCT 1000
334 IAspIleuSerGlyIleuThrAlaArgGluTyrAlaValSerSerHis 350
  |||
1001 AAGATCTATCTGACAGACAGCGCCAGAGATATGCTGTTCTAGTAT 1050
351 HisValIleCysGlnIleuIleuSerAspTyrIyGlnIyGlnMetIle 367
  |||
1051 CATCTAATTTGCCAGTACTTCTGTACTCAAAAGAAAAAGATGCTTAA 1100
367 sIleSerSerGluAsnSerAsnProGluAsnValSerArgThrArgAs 384
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1101 AATCTCTTCTGAAACACGATCAGAAATATGTCATCAAGACCAATA 1150
384 yS 384
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1151 AA 1152

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seq\_name: /SDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.AAC81012

seq\_documentation\_block:  
 ID AAC81012 standard; CDNA; 2000 BP.  
 XX  
 AC AAC81012;  
 XX  
 DT 13-FEB-2001 (first entry)  
 XX  
 DE Human B1Agl antigen splice isoform B1A-8 cDNA.  
 XX  
 KW Human; breast tumour-specific antigen; cytostatic; vaccine;  
 KW breast cancer; B1Agl; B1Agl; B1Agl; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200061753-A2.  
 XX  
 FD 19-OCT-2000.  
 XX  
 PF 07-APR-2000; 2000MO-0509312.  
 XX  
 PR 09-APR-1999; 99US-0289198.  
 PR 28-OCT-1999; 99US-0429755.  
 PR 23-MAR-2000; 2000US-0534825.  
 XX  
 PA (COR1-) COR1A CORP.  
 XX  
 PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;  
 XX  
 DR WPI: 2000-628403/60.  
 DR P-PSDB: AAB28629.  
 XX  
 PT An isolated polypeptide comprising an immunogenic portion of a breast  
 PT tumor protein used for inhibiting the development of cancer, especially  
 PT breast cancer, and monitoring cancer progression in a patient -  
 XX  
 PS Claim 4; Page 177-178; 187pp; English.  
 XX  
 CC The present sequence is given in a specification relating to compositions  
 CC and methods for the treatment and diagnosis of breast cancer. Nucleotide





DE Human prostate cDNA clone B305D splice variant #9.

KM Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.

OS Homo sapiens.

PN W0200173032-A2.

PD 04-OCT-2001.

PF 27-MAR-2001; 2001WO-US09919.

PR 27-MAR-2000; 2000US-0536857.

PR 09-MAY-2000; 2000US-0568100.

PR 12-MAY-2000; 2000US-0570737.

PR 13-JUN-2000; 2000US-0593793.

PR 27-JUN-2000; 2000US-0605783.

PR 10-AUG-2000; 2000US-0636213.

PR 29-AUG-2000; 2000US-0651236.

PR 06-SEP-2000; 2000US-0657279.

PR 02-OCT-2000; 2000US-0679426.

PR 10-OCT-2000; 2000US-0685166.

XX (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker ST, Jiang Y, Kaios MD;

PI Panger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;

DR WPI: 2001-639232/73.

DR P-PSDB; AAU69378.

XX New human prostate-specific polypeptides and polynucleotides useful for

PT the diagnosis and treatment of cancer, especially prostate cancer -

PS Claim 1: Page 349-350; 579pp; English.

XX The invention relates to isolated prostate-specific

CC polynucleotides, polypeptides, fusion proteins of the polypeptides,

CC antibodies raised against the polypeptides (or antigenic epitopes

CC derived from them) and antigen-presenting cells expressing the

CC polypeptides. The antibodies are useful for detecting the presence of

CC cancer, especially prostate cancer. The polypeptides, polynucleotides and

CC T cells specific for a tumour protein, and for inhibiting the development

CC of cancer especially prostate cancer. Compositions comprising the

CC polynucleotide and/or polypeptide are useful for stimulating an immune

CC response, and for treating cancer. The oligonucleotide is useful for

CC detecting cancer. The present sequence is a prostate specific

CC polynucleotide of the invention.

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

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Quality: 2024.00 Length: 376

Ratio: 5.383 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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51 ATTGGCTTCAGAGCAAGATGGCGAAGTGGTGGCTGGCTTCCCTC 100

34 yscYsArgGluSerGlyLysSerAsnValGlyThrSerGlyAspHisAsp 50

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317 ValSerLysLeuValSerLeuLeuGluGlnAsnLysAspValSerSerG 334  
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334 LysPheSerGlyLysThrAlaArgGlyLysValValSerSerHisHis 350





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 317 AlaSerIleValSerLeuLeuGluGlnAsnIleAspValSerSerG 334  
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ID AAH85029 standard; cDNA; 2000 BP.

XX AAH85029;

XX 25-SEP-2001 (first entry)

XX Human prostate-specific cDNA sequence B305D splice variant #9.

XX Human prostate cancer; therapy; diagnosis; cat eye syndrome;

KM chromosome 22q11.2; prostate-specific protein; chromosome 1;

XX prostate specific antigen; PSA; ss.

OS Homo sapiens.

XX WO200134802-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US30904.

XX 12-NOV-1999; 99US-0439313.

XX 18-NOV-1999; 99US-0443686.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;

XX WPI; 2001-308785/32.

XX Isolated polypeptide comprising at least an immunogenic portion of a

PT prostate-specific protein, useful in the diagnosis and therapy of a

XX prostate cancer -

XX Claim 31: Page 247-248; 325pp; English.

XX The present invention describes an isolated polypeptide (P1) comprising

CC at least an immunogenic portion of a prostate-specific protein, or its

CC variant. Also described are polynucleotides (N1) encoding (P1) and

CC (N1) have cytostatic activity and can be used in vaccine production.

CC The polypeptides, nucleic acids and antibodies from the present

CC invention are useful in the diagnosis and therapy of prostate cancer.

CC Prostate specific genes PT04P, P712P, P774P, P775P and R305P are located

CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome

CC region. Prostate specific antigen (PSA) P501S was located on

CC chromosome 1. AAH84671 to AAH85143 and AA69900 to AA69977 represent

CC polynucleotide and polypeptide sequences used in the exemplification

CC of the present invention.

XX SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

alignment\_scores:

Quality: 2024.00 Length: 376  
 Ratio: 5.383 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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 34 YsCysArgGluSerGlyIleSerSerValGlyThrSerGlyIleAsp 50  
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 67 sCysPheProCysArgGlySerGlyIleSerSerValGlyIleAsp 84  
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 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bcrf-mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
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Yamamoto,O., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3851
Fax: 81-438-52-3852
Email: genomese@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
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DNA Sequencing by: Incyte Genomics, Inc.
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http://image.llnl.gov
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## TITLE

Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
Tanaka, T., Tejima, T., Toya, T., Yamamura, T., Yamana, I.,  
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and  
Hayashizaki, Y.

## Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
Kanagawa 230-0045, Japan (E-mail: genome\_res@gscc.riken.go.jp,  
URI: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## COMMENT

Please visit our web site (http://genome.gsc.riken.go.jp/) for  
further details.

## FEATURES

## source

Location/Qualifiers  
1. 1758  
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/strain="C57BL/6J"  
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/clone\_1lb="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="8 days embryo"  
159. >1758  
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putative"

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SMAKILAHANAEKKNKDIIPMLIAVKEKQHTVEFLYKKASITAHVODLSRDM  
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BASE COUNT 531 a 392 c 474 g 361 t  
ORIGIN

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Quality: 521.50 Length: 386  
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Percent similarity: 52.073 Percent identity: 34.456

## alignment\_block:

us-09-810-936-304 x AK017783 ..

Align seg 1/1 to: AK017783 from: 1 to: 1758

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19 YLeuATSerLysMetGlyLysTrpCysGlyArgSpheProCysGly 36
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176 CTTGAGGAGTAG..... 188
36 rgluSerGlyLysSerAsnValGlyThrSerGlyAspHisAspAspSer 52
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53 AlawetLysThrLeuArgSerLysMetGlyLysTrpCysArgHisCysPh 69
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69 eProCysCysArgGlySerGlyLysSerAsnValGlyLysSerGlyAspH 86
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231 .....TGCCTGGCTTTGAGCGGAGAGT.....GCTAGTGGCTGCC 267
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268 AC..... 269
103 CysHisCysPheProCysGlyArgGlySerGlyLysSerLysValGlyAl 119
269 ..... 269
119 aTrpGlyAspTrpAspAspSerAlaPheMetGlyProArgTrpHisValA 136
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270 .....GTGCCCATGATCCATATTC..... 288
136 rglGlyLysAspLysLysLysLeuHisArgAlaAlaTrpTrpGlyLysVal 152
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153 ProArgLysAspLeuIleValMetLeuArgAspThrAspValAsnLysL 169
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339 GCCAAAGTCCAGCATATCCCTATTCCTTGAAAAGATGCGCTGAACGATAG 388
169 sAspLysGlnLysArgThrAlaLeuHisLeuAlaSerAlaAsnGlyAsnS 186
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389 AGCAAGAAAGACAGACAGACTGCTGACATCTTGCGCTTGACGGCCACC 438
186 eArgLysValLysLeuLeuLeuAspArgArgCysGlnLeuAsnValLeu 202
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439 CAGAAAGTGTGACTCTCTTAATGAGAGAAAATGTGAATATGATGCCCTG 488
203 AspAsnLysLysArgThrAlaLeuIleLysAlaValAlaGlnCysGlnLys 219
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489 GACAGGAGAGCAGCAGCGCCCTCATTAAGCCCTGACAGTGCACGAGGAGA 538
219 rglCysArgAlaLeuMetLeuGlnHisGlyThrAspProAsnLysProA 236
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253 LeuMetAlaLysAlaLeuLeuLeuTrpGlyAlaAspIleGlySerLysAs 269
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286 InValLysPheLeuIleLysLysLysAlaAsnLeuAsnAlaLeuAsp 302
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739 ATATGTGGAAATTTTATGTAAGAAAGAAACCAAGATATCAGCAGTTGAT 788
303 ArgTrpGlyArgThrAlaLeuIleLeuAlaValCysCysGlySerAlaSe 319
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789 CAGCTTGG..... 797
319 rIleValSerLeuLeuLeuGlnGlnAsnIleAspValSerSerGlnAsp 336
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797 ..... 797
336 euSerGlyGlnThrAlaArgGlyTrpAlaValSerSerHisHisValA 352
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798 .ACCAACAGCGCAAAATGTTGAAAT..... 821
353 IleCysGlnLeuLeuSerAspTrpLysGlnLysGlnMetLeuLysIleSe 369
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822 .....GATGGAAGAGACTACAA.....AG 841
369 rSerGlnAsnSerAsnPro.....GluAsnValSerArgT 381
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842 ATCTGAACAAACGAAATCCAGTGATATATGTTCTGAAGATGCTCTTAA 891
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127 .....AlaPheMetLuro..... 131
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132 ..ATGTyrHisValArGgLYGLuAspLeuAspLysLeuHisArgAlaLa 147
225 GAGATATTCGCTTCGAGATAGCACTTAAGAACTTCATTAACCTCT 274
148 TrpTrpGlyValProArGlyAspLeuIleValMetLeuArgAspTh 164
275 ACCATTGGCAATAGCAGCAAGCTGAAGATTACTTGAACGCAAAATA 324
164 rAspValAsnLysLysAspLysGlnLysArgThrAlaLeuHisLeuAla 181
325 CAATGTGAATGGCGGACAAAGAGACAGAACCTTGCTTGCGCT 374
181 erAlaAsnGlyAsnSerGluValValLysLeuLeuLeuAspArgArgCys 197
375 GTGTGTGGATATACAAATATGTCTCTCTTAATGAGATCAATGC 424
198 GlnLeuAsnValLeuAspAsnLysLysArgThrAlaLeuIleLysAla 214
425 AAATTTATGTCCAGTACTGAAACAGACCCATTCATTAAGCAGT 474
214 LGlncGlyGlnLusAspGluCysAlaLeuMetLeuGluHisGlyThra 231
475 AGAGTGTCAACAGGAGTGTGTACGGTCTCTCTTCACAGGTGAG 524
231 sPrProAsnIleProAspGluTyrGlyAsnThrThrLeuHisTyrAlaIle 247
525 ATCAAAATGTGTAGATGTTATAGTAATACGCGCTCCATATAGCTGT 574
248 TyrAsnGluAspLysLeuMetAlaValAlaLeuLeuTyrGlyAlaAs 264
575 TGTGGCCCAAAATATTCATTAAGCAAAATGCTTCATTAAGCCAA 624
264 pIleGluSerLysAsnLysHisGlyLeuThrProLeuLeuGluGlyValH 281
625 TCTTGAAGCCAAATATAGAGCGTCACACTCGGCTTTACTGCTGTG 674
281 tSgGluGlnLysGlnGlnValValLysPheLeuIleLysLysAlaAsn 297
675 CTGAATAATGAATAATATGTAAATTCCTCTGAAGAAAGACAGAT 724
298 LeuAsnAlaLeuAspArgTyrGlyArgThrAlaLeuIleLeuAlaValCy 314
725 GTAATATGATCAGATMAAACACAGACACGATCATGATGCTGTAT 774
314 sCyGgLYSerAlaSerIleValSerLeuLeuGluGlnAsnIleAspV 331
775 TGTGAACCAACAAGTCTGTAAACTTCTCTCAAGCAAGATAGGAGC 824
331 alSerSerGlnAspLeuSerGlyGlnThrAlaArgGluTyrAla..... 345
825 TAGCCCAACAAGATATTATGATTACAGCTGAGGAATATGCTTCATT 874
346 .....ValSerSerHisHisValIleCyGlnLeuLeuSerAspTy 360
875 AATGGCTTACTATGTATCCACAT..... 898
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ACCESSION  Bg720647
VERSION    Bg720647.1  GI:13999834
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 694)
            NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgraps-remail.nih.gov
COMMENT     Tissue procurement: Miklos Palkovits, M.D., Ph.D.
            CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
            Toshiyuki and Piero Carninci (RIKEN)
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLNL0736 row: h column: 07
            High quality sequence stop: 694.
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                size-selected for average insert size 2.2 kb and
                normalized to ROT 5. This is a primary library enriched
                for full-length clones and constructed using the
                Cap-trapper method (Carninci, in preparation). Library
                constructed by M. Brownstein (NIH/NHGRI, National
                Institutes of Health). Note: this is a NIH-MGC Library."
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ORIGIN
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US-09-810-936-304 x Bg720647 ..
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51 AspSerAlaMetLysThrLeuArgSerLysMetGlyLysTyrPCysArgH 67
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526 GACATCTTATGAGAGCGCTCAGAGACAGAGATGGCAAGTGTGGCACCA 575

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TITLE
JOURNAL
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15' GAGGAGAGACGATCCAGAGCCTCTTTTCTTTTTTTTTTNN 3', cDNA was prepared by using trichloroethanol thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGGAGAGATTCGGATTAAATTAATTAATCCCCCCCCCCC 3'. cDNA was cleaved with BamHI and XhoI. Vector: a modified pluescript KS(+) after bulk excision from Lambda FIC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
FEATURES
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/translat="MKRTIFGAKEKPLGFQDAOMTVSEFEGENPNPKYHTTYRLGHIAVAEGDAARMEILFLGOENVYHRDKRALRHACYGLRPVTLIVNKEELIDALKNHTPIPMKSVOCKOKCATVLEHGDPRNRSSGSADLHVDELORTLTAYIRLLIOANNAIEOKTKDGFTPLLAKREKVAEAFVLRMGAADIHHVDORNTLTAYIRCGRSLSTILLERGISDFYDVFGMTALRAIEHGKTFRQTLLDFEESLNKKDKRRPELVQRVSTCLAKQIDAGNDSTARISCPSPETPVLIWKEDNSDAHVNCSVELLPWKPVEFGLE"
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ORIGIN
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Percent Similarity: 74.297 Percent Identity: 40.964
alignment_block:
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Align seg 1/1 to: AKO15165 from: 1 to: 1400
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264 CGGAATAACCATCAACATCACAGCCGTGGGCGCATATTTCACAGCGTGCC 313
147 atrrtgclylvysvalproatrglyspleulevalmetetuegraspr 164
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JOURNAL MEDLINE	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	99279253
REFERENCE	10349636
AUTHORS	2 (sites) Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,H., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	20499374
REFERENCE	11042159
AUTHORS	3 (sites) Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,T., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiyagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kirita,A. and Hayashizaki,Y.
TITLE	Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	20530913
REFERENCE	11076861
AUTHORS	4 (sites) The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL MEDLINE	Nature 409, 685-690 (2001)
REFERENCE	5 (bases 1 to 1441)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Anono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bull,C., Carninci,P., Fukuda,S., Fukushima,F., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiroka,T., Horii,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kono,H., Kouda,M., Koyra,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numezaki,R., Ono,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sobabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGACGAGAGCGAGTAAATTAATAAATCCCCCCC 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGACGAGTTCGAGTTAAATTAATAAATCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from lambda Phi C I. Cloning sites, 5' end: Salt; 3' end: BamHI. Host: DH109.
FEATURES	location/Qualifiers 1..1441 /organism="Mus musculus" /strain="C57BL/6J"







0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note this is a NIH MGC Library."

BASE COUNT	259 a	151 c	196 g	222 t
ORIGIN				

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  Ratio: 2.907         Gaps: 1
Percent Similarity: 76.056      Percent Identity: 46.009

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alignment\_block:  
US-09-810-936-304 x BI827177

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 149 pGlyValProArgIleAspLeuIleValMetLeuArgAspHisArg 166  
 150 :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::  
 151 CGGGGATTATGAGACCTGACAGGAATACCTTGACGTACGATAGAAATATATGT 205  
 166 AlaLeuLysAspLysGlnLysArgThrAlaLeuHisIleAlaSerAla 182  
 167 :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::  
 168 TAAATATGCGGACCAAAAATACAGACACCTTTGGACACGTGCTGTCTT 305  
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 233 AsnIleProAspGlnLysGlnSerThrIleHisIleValIleLysArg 249  
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 268 AAGCGAAATATAGATGGGTATCTCCACCTTGTAGTGCCTATTATAC 605  
 283 GlnLysGlnIleValValLysPheLeuIleLysLysLysAlaAsnLeuAs 299  
 284 :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::  
 285 AATATATCCAAAATGGTAAATTTCTTCTGAGAAAGGGCGCTGATGGAA 655  
 299 AlaLeuAspArgTyrGlyArgThrAlaLeuIleLeuAlaValCysCysG 316  
 300 :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::  
 301 TGCCTTCAGATAAATTAACAAGACAGCCCTTATCTTCTGCTCAGTGTG 705  
 316 LysSerAlaSerIleValSerLeuLeuLeuGlnGlnAsnIleAspValSer 332  
 317 :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::  
 318 AATCACCATGTTATGTAAGCTTCTTCTTACACAAAGTGTGCGCAATTCAT 755  
 333 SerGlnAspLeuSer GlyGlnThrAlaArgGlnTyr 344  
 334 :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::  
 335 GTTATCGAAGGTATTCGTGGATTCACAGCTAGGAGAAAT 792

```
seq_name: gb_hlc:AK005925
seq_documentation_block:
```

LOCUS	1209 bp	MRNA	linear	HFC 19-JAN-2000
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:11700012M14:ANKRYIN-LIKE PROTEIN, full insert sequence.			
ACCESSION	AK005925			
VERSION	AK005925.1			
KEYWORDS	HFC; CAP trapper.			
SOURCE	Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone:11b:RIKEN full-length enriched mouse cDNA library			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Garninci,P. and Hayashizaki,Y.			
TITLE	High efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
PMID	99279253			
PMID	10349636			
REFERENCE	2 (sites)			
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
PMID	20493374			
PMID	11042159			
REFERENCE	3 (sites)			
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komoto,H., Akiyama,J., Nishi,K., Kitsuami,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishue,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiki,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoshida,Y., Ishikawa,T., Ozawa,K., Tanaka,T. and Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
PMID	20530913			
PMID	11076861			
REFERENCE	4 (sites)			
AUTHORS	The Riken Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
PMID	5 (phases 1 to 1203)			
PMID	11076861			
REFERENCE	Aaachi,Y., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arawaka,T., Badatelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hitamoto,K., Hiroaka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shimizu,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogaue,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,I., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamashita,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 220-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)			
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for			









